

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/802,755A

DATE: 08/01/2001
TIME: 14:18:05

Input Set : A:\2555-001.ST25.txt
Output Set: N:\CRF3\08012001\I802755A.raw

ENTERED

3 <110> APPLICANT: Darst, Seth A
4 Campbell, Elizabeth A.
6 <120> TITLE OF INVENTION: CRYSTAL OF BACTERIA CORE RNA POLYMERASE WITH RIFAMPICIN
8 <130> FILE REFERENCE: 2555-1-001
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/802,755A
11 <141> CURRENT FILING DATE: 2001-03-09
13 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1525
19 <212> TYPE: PRT
20 <213> ORGANISM: Thermus aquaticus
22 <220> FEATURE:
23 <221> NAME/KEY: MISC_FEATURE
24 <222> LOCATION: (1247)...(1247)
25 <223> OTHER INFORMATION: Xaa can be any amino acid.
28 <400> SEQUENCE: 1
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31 1 5 10 15
34 Lys Ile Arg Ser Trp Ser Tyr Gly Glu Val Glu Lys Pro Glu Thr Ile
35 20 25 30
38 Asn Tyr Arg Thr Leu Lys Pro Glu Arg Asp Gly Leu Phe Asp Glu Arg
39 35 40 45
42 Ile Phe Gly Pro Ile Lys Asp Tyr Glu Cys Ala Cys Gly Lys Tyr Lys
43 50 55 60
46 Arg Gln Arg Phe Glu Gly Lys Val Cys Glu Arg Cys Gly Val Glu Val
47 65 70 75 80
50 Thr Arg Ser Ile Val Arg Arg Tyr Arg Met Gly His Ile Glu Leu Ala
51 85 90 95
54 Thr Pro Ala Ala His Ile Trp Phe Val Lys Asp Val Pro Ser Lys Ile
55 100 105 110
58 Gly Thr Leu Leu Asp Leu Phe Ala Thr Glu Leu Glu Gln Val Leu Tyr
59 115 120 125
62 Phe Asn Lys Tyr Ile Val Leu Asp Pro Lys Gly Ala Val Leu Asp Gly
63 130 135 140
66 Val Pro Val Glu Lys Arg Gln Leu Leu Thr Asp Glu Glu Tyr Arg Glu
67 145 150 155 160
70 Leu Arg Tyr Gly Lys Gln Glu Thr Tyr Pro Leu Pro Ala Gly Val Asp
71 165 170 175
74 Ala Leu Val Lys Asp Gly Glu Glu Val Val Lys Gly Gln Glu Leu Ala
75 180 185 190
78 Pro Gly Val Val Ser Arg Met Asp Gly Val Gly Ser Leu Pro Leu Pro
79 195 200 205
82 Arg Arg Val Arg Val Asp Tyr Leu Arg Lys Glu Arg Ala Ala Leu Arg
83 210 215 220
86 Ile Pro Leu Ser Ala Trp Val Glu Lys Glu Pro Tyr Arg Pro Gly Glu
87 225 230 235 240

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90 Val Leu Ala Glu Leu Ser Glu Pro Tyr Leu Phe Arg Ala Glu Glu Ser
91           245          250          255
94 Gly Val Val Glu Leu Lys Asp Leu Ala Glu Gly His Leu Ile Tyr Leu
95           260          265          270
98 Arg Gln Glu Glu Val Val Ala Arg Tyr Phe Leu Pro Ala Gly Met
99           275          280          285
102 Thr Pro Leu Val Val Glu Gly Glu Ile Val Glu Val Gly Gln Pro Leu
103          290          295          300
106 Ala Glu Gly Lys Gly Leu Leu Arg Leu Pro Arg His Met Thr Ala Lys
107          305          310          315          320
110 Glu Val Glu Ala Glu Glu Gly Asp Ser Val His Leu Thr Leu Phe
111           325          330          335
114 Leu Glu Trp Thr Glu Pro Lys Asp Tyr Lys Val Ala Pro His Met Asn
115           340          345          350
118 Val Ile Val Pro Glu Gly Ala Lys Val Gln Ala Gly Glu Lys Ile Val
119           355          360          365
122 Ala Ala Ile Asp Pro Glu Glu Glu Val Ile Ala Gln Ala Glu Gly Val
123           370          375          380
126 Val His Leu His Glu Pro Ala Ser Ile Leu Val Val Lys Ala Arg Val
127          385          390          395          400
130 Tyr Pro Phe Glu Asp Asp Val Glu Val Thr Thr Gly Asp Arg Val Ala
131           405          410          415
134 Pro Gly Asp Val Leu Ala Asp Gly Gly Lys Val Lys Ser Glu Ile Tyr
135           420          425          430
138 Gly Arg Val Glu Val Asp Leu Val Arg Asn Val Val Arg Val Val Glu
139           435          440          445
142 Ser Tyr Asp Ile Asp Ala Arg Met Gly Ala Glu Ala Ile Gln Glu Leu
143           450          455          460
146 Leu Lys Glu Leu Asp Leu Glu Lys Leu Glu Arg Glu Leu Leu Glu Glu
147          465          470          475          480
150 Met Lys His Pro Ser Arg Ala Arg Arg Ala Lys Ala Arg Lys Arg Leu
151           485          490          495
154 Glu Val Val Arg Ala Phe Leu Asp Ser Gly Asn Arg Pro Glu Trp Met
155           500          505          510
158 Ile Leu Glu Ala Val Pro Val Leu Pro Pro Asp Leu Arg Pro Met Val
159           515          520          525
162 Gln Val Asp Gly Gly Arg Phe Ala Thr Ser Asp Leu Asn Asp Leu Tyr
163           530          535          540
166 Arg Arg Leu Ile Asn Arg Asn Asn Arg Leu Lys Lys Leu Leu Ala Gln
167          545          550          555          560
170 Gly Ala Pro Glu Ile Ile Ile Arg Asn Glu Lys Arg Met Leu Gln Glu
171           565          570          575
174 Ala Val Asp Ala Val Ile Asp Asn Gly Arg Arg Gly Ser Pro Val Thr
175           580          585          590
178 Asn Pro Gly Ser Glu Arg Pro Leu Arg Ser Leu Thr Asp Ile Leu Ser
179           595          600          605
182 Gly Lys Gln Gly Arg Phe Arg Gln Asn Leu Leu Gly Lys Arg Val Asp
183           610          615          620
186 Tyr Ser Gly Arg Ser Val Ile Val Val Gly Pro Gln Leu Lys Leu His

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187	625	630	635	640
190	Gln Cys Gly Leu Pro Lys Arg Met Ala Leu Glu Leu Phe Lys Pro Phe			
191		645	650	655
194	Leu Leu Lys Lys Met Glu Glu Lys Ala Phe Ala Pro Asn Val Lys Ala			
195		660	665	670
198	Ala Arg Arg Met Leu Glu Arg Gln Arg Asp Ile Lys Asp Glu Val Trp			
199		675	680	685
202	Asp Ala Leu Glu Glu Val Ile His Gly Lys Val Val Leu Leu Asn Arg			
203		690	695	700
206	Ala Pro Thr Leu His Arg Leu Gly Ile Gln Ala Phe Gln Pro Val Leu			
207		705	710	715
210	Val Glu Gly Gln Ser Ile Gln Leu His Pro Leu Val Cys Glu Ala Phe			
211		725	730	735
214	Asn Ala Asp Phe Asp Gly Asp Gln Met Ala Val His Val Pro Leu Ser			
215		740	745	750
218	Ser Phe Ala Gln Ala Glu Ala Arg Ile Gln Met Leu Ser Ala His Asn			
219		755	760	765
222	Leu Leu Ser Pro Ala Ser Gly Glu Pro Leu Ala Lys Pro Ser Arg Asp			
223		770	775	780
226	Ile Ile Leu Gly Leu Tyr Tyr Ile Thr Gln Val Arg Lys Glu Lys Lys			
227		785	790	795
230	800	805	810	815
234	Gly Ala Gly Met Ala Phe Ala Thr Pro Glu Glu Ala Leu Ala Ala Tyr			
235		820	825	830
238	Glu Thr Ser Val Gly Arg Leu Lys Phe Val Phe Ala Asn Pro Asp Glu			
239		835	840	845
242	Ala Leu Leu Ala Val Ala His Gly Leu Leu Asp Leu Gln Asp Val Val			
243		850	855	860
246	247	865	870	875
250	Thr Val Arg Tyr Leu Gly Arg Arg Leu Glu Thr Asn Pro Gly Arg Ile			
251		885	890	895
254	Leu Phe Ala Arg Ile Val Gly Glu Ala Val Gly Asp Glu Lys Val Ala			
255		900	905	910
258	Gln Glu Leu Ile Gln Met Asp Val Pro Gln Glu Lys Asn Ser Leu Lys			
259		915	920	925
262	Asp Leu Val Tyr Gln Ala Phe Leu Arg Leu Gly Met Glu Lys Thr Ala			
263		930	935	940
266	Arg Leu Leu Asp Ala Leu Lys Tyr Tyr Gly Phe Thr Leu Ser Thr Thr			
267		945	950	955
270	Ser Gly Ile Ile Thr Ile Gly Ile Asp Asp Ala Val Ile Pro Glu Glu			
271		965	970	975
274	Lys Gln Arg Tyr Leu Glu Glu Ala Asp Arg Lys Leu Arg Gln Ile Glu			
275		980	985	990
278	Gln Ala Tyr Glu Met Gly Phe Leu Thr Asp Arg Glu Arg Tyr Asp Gln			
279		995	1000	1005
282	Val Ile Gln Leu Trp Thr Glu Thr Thr Glu Lys Val Thr Gln Ala Val			
283		1010	1015	1020

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286 Met Ala Gln Ser Gly Ala Arg Gly Asn Pro Gln Gln Ile Arg Gln
 287 1025 1030 1035
 290 Leu Cys Gly Met Arg Gly Leu Met Gln Lys Pro Ser Gly Glu Thr
 291 1040 1045 1050
 294 Phe Glu Val Pro Val Arg Ser Ser Phe Arg Glu Gly Leu Thr Val
 295 1055 1060 1065
 298 Leu Glu Tyr Phe Ile Ser Ser His Gly Ala Arg Lys Gly Gly Ala
 299 1070 1075 1080
 302 Asp Thr Ala Leu Arg Thr Ala Asp Ser Gly Tyr Leu Thr Arg Lys
 303 1085 1090 1095
 306 Leu Val Asp Val Ala His Glu Ile Val Val Arg Glu Ala Asp Cys
 307 1100 1105 1110
 310 Gly Thr Thr Lys Tyr Ile Ser Val Pro Leu Phe Gln Met Asp Glu
 311 1115 1120 1125
 314 Val Thr Arg Thr Leu Arg Leu Arg Lys Arg Ser Asp Ile Glu Ser
 315 1130 1135 1140
 318 Gly Leu Tyr Gly Arg Val Leu Ala Arg Glu Val Glu Ala Leu Gly
 319 1145 1150 1155
 322 Arg Arg Leu Glu Glu Gly Arg Tyr Leu Ser Leu Glu Asp Val His
 323 1160 1165 1170
 326 Phe Leu Ile Lys Ala Ala Glu Ala Gly Glu Val Arg Glu Val Pro
 327 1175 1180 1185
 330 Val Arg Ser Pro Leu Thr Cys Gln Thr Arg Tyr Gly Val Cys Gln
 331 1190 1195 1200
 334 Lys Cys Tyr Gly Tyr Asp Leu Ser Met Ala Arg Pro Val Ser Ile
 335 1205 1210 1215
 338 Gly Glu Ala Val Gly Val Val Ala Ala Glu Ser Ile Gly Glu Pro
 339 1220 1225 1230
 342 Gly Thr Gln Leu Thr Met Arg Thr Phe His Thr Gly Gly Xaa Ala
 343 1235 1240 1245
 346 Val Gly Thr Asp Ile Thr Gln Gly Leu Pro Arg Val Ile Glu Leu
 347 1250 1255 1260
 350 Phe Glu Ala Arg Arg Pro Lys Ala Lys Ala Val Ile Ser Glu Ile
 351 1265 1270 1275
 354 Asp Gly Val Val Arg Ile Glu Glu Gly Glu Asp Arg Leu Ser Val
 355 1280 1285 1290
 358 Phe Val Glu Ser Glu Gly Phe Ser Lys Glu Tyr Lys Leu Pro Lys
 359 1295 1300 1305
 362 Asp Ala Arg Leu Leu Val Lys Asp Gly Asp Tyr Val Glu Ala Gly
 363 1310 1315 1320
 366 Gln Pro Leu Thr Arg Gly Ala Ile Asp Pro His Gln Leu Leu Glu
 367 1325 1330 1335
 370 Ala Lys Gly Pro Glu Ala Val Glu Arg Tyr Leu Val Asp Glu Ile
 371 1340 1345 1350
 374 Gln Lys Val Tyr Arg Ala Gln Gly Val Lys Leu His Asp Lys His
 375 1355 1360 1365
 378 Ile Glu Ile Val Val Arg Gln Met Leu Lys Tyr Val Glu Val Thr
 379 1370 1375 1380
 382 Asp Pro Gly Asp Ser Pro Leu Leu Glu Gly Gln Val Leu Glu Lys

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Input Set : A:\2555-001.ST25.txt

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383	1385	1390	1395	
386	Trp Asp Val Glu Ala Leu Asn	Glu Arg Leu Ile Ala	Glu Gly Lys	
387	1400	1405	1410	
390	Val Pro Val Ala Trp Lys	Pro Leu Leu Met Gly Val	Thr Lys Ser	
391	1415	1420	1425	
394	Ala Leu Ser Thr Lys Ser	Trp Leu Ser Ala Ala Ser	Phe Gln Asn	
395	1430	1435	1440	
398	Thr Thr His Val Leu Thr	Glu Ala Ala Ile Ala	Gly Lys Lys Asp	
399	1445	1450	1455	
402	Glu Leu Ile Gly Leu Lys	Glu Asn Val Ile Leu	Gly Arg Leu Ile	
403	1460	1465	1470	
406	Pro Ala Gly Thr Gly Ser	Asp Phe Val Arg Phe	Thr Gln Val Val	
407	1475	1480	1485	
410	Asp Gln Arg Thr Leu Lys	Ala Ile Glu Glu Ala Arg	Lys Glu Ala	
411	1490	1495	1500	
414	Val Glu Ala Lys Glu Lys	Glu Ala Pro Arg Arg	Pro Val Arg Arg	
415	1505	1510	1515	
418	Glu Gln Pro Gly Lys Gly	Leu		
419	1520	1525		
422	<210> SEQ ID NO: 2			
423	<211> LENGTH: 1119			
424	<212> TYPE: PRT			
425	<213> ORGANISM: Thermus aquaticus			
427	<220> FEATURE:			
428	<221> NAME/KEY: MISC_FEATURE			
429	<222> LOCATION: (695)..(696)			
430	<223> OTHER INFORMATION: Xaa can be any amino acid			
433	<220> FEATURE:			
434	<221> NAME/KEY: MISC_FEATURE			
435	<222> LOCATION: (1247)..(1247)			
436	<223> OTHER INFORMATION: Xaa can be any amino acid			
439	<400> SEQUENCE: 2			
441	Met Lys Ile Lys Arg Phe Gly Arg Ile Arg Glu Val Ile Pro Leu Pro			
442	1	5	10	15
445	Pro Leu Thr Glu Ile Gln Val Glu Ser Tyr Lys Lys Ala Leu Gln Ala			
446	20	25	30	
449	Asp Val Pro Pro Glu Lys Arg Glu Asn Val Gly Ile Gln Ala Ala Phe			
450	35	40	45	
453	Lys Glu Thr Phe Pro Ile Glu Glu Gly Asp Lys Gly Lys Gly Leu			
454	50	55	60	
457	Val Leu Asp Phe Leu Glu Tyr Arg Ile Gly Asp Pro Pro Phe Ser Gln			
458	65	70	75	80
461	Asp Glu Cys Arg Glu Lys Asp Leu Thr Tyr Gln Ala Pro Leu Tyr Ala			
462	85	90	95	
465	Arg Leu Gln Leu Ile His Lys Asp Thr Gly Leu Ile Lys Glu Asp Glu			
466	100	105	110	
469	Val Phe Leu Gly His Leu Pro Leu Met Thr Glu Asp Gly Ser Phe Ile			
470	115	120	125	
473	Ile Asn Gly Ala Asp Arg Val Ile Val Ser Gln Ile His Arg Ser Pro			

→ Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/802,755A

DATE: 08/01/2001

TIME: 14:18:06

Input Set : A:\2555-001.ST25.txt

Output Set: N:\CRF3\08012001\I802755A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2